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SEQUENCE LISTING

A1
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McGill University

<120> DNA ENCODING A HUMAN PROTON-GATED ION CHANNEL AND USES
THEREOF

<130> 641050.90021

<140> CA PCT/CA98/01016

<141> 1998-10-29

<150> US09/530,233

<151> 1997-10-29

<160> 5

<170> PatentIn Ver. 2.0

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<211> 1732

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cgg cgg cag ccc tcg gac atc cgc gtg ttc gcc agc aac tgc tcg atg 99
Arg Arg Gln Pro Ser Asp Ile Arg Val Phe Ala Ser Asn Cys Ser Met
15 20 25

cac ggg ctg ggc cac gtc ttc ggg cca ggc agc ctg agc ctg cgc cgg 147
His Gly Leu Gly His Val Phe Gly Pro Ser Leu Ser Leu Arg Arg
30 35 40

ggg atg tgg gca gcg gcc gtg gtc ctg tca gtg gcc acc ttc ctc tac 195
Gly Met Trp Ala Ala Ala Val Val Leu Ser Val Ala Thr Phe Leu Tyr
45 50 55

cag gtg gct gag agg gtg cgc tac tac agg gag ttc cac cac cag act 243

Gln	Val	Ala	Glu	Arg	Val	Arg	Tyr	Tyr	Arg	Glu	Phe	His	His	Gln	Thr	
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gcc ctg gat gag cga gaa agc cac cgg ctc gtc ttc ccg gct gtc acc															291	
Ala	Leu	Asp	Glu	Arg	Glu	Ser	His	Arg	Leu	Val	Phe	Pro	Ala	Val	Thr	
75					80					85					90	
ctg tgc aac atc aac cca ctg cgc cgc tcg cgc cta acg ccc aac gac															339	
Leu	Cys	Asn	Ile	Asn	Pro	Leu	Arg	Arg	Ser	Arg	Leu	Thr	Pro	Asn	Asp	
					95					100					105	
ctg cac tgg gct ggg tct gcg ctg ggc ctg gat ccc gca gag cac															387	
Leu	His	Trp	Ala	Gly	Ser	Ala	Leu	Leu	Gly	Leu	Asp	Pro	Ala	Glu	His	
					110					115					120	
gcc gcc ttc ctg cgc gcc ctg ggc cgg ccc cct gca ccg ccc ggc ttc															435	
Ala	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Arg	Pro	Pro	Ala	Pro	Pro	Gly	Phe	
					125					130					135	
atg ccc agt ccc acc ttt gac atg gcg caa ctc tat gcc cgt gct ggg															483	
Met	Pro	Ser	Pro	Thr	Phe	Asp	Met	Ala	Gln	Leu	Tyr	Ala	Arg	Ala	Gly	
					140					145					150	
cac tcc ctg gat gac atg ctg gac tgt cgc ttc cgt ggc caa cct															531	
His	Ser	Leu	Asp	Asp	Met	Leu	Leu	Asp	Cys	Arg	Phe	Arg	Gly	Gln	Pro	
					155					160					165	
tgt ggg cct gag aac ttc acc acg atc ttc acc cgg atg gga aag tgc															579	
Cys	Gly	Pro	Glu	Asn	Phe	Thr	Thr	Ile	Phe	Thr	Arg	Met	Gly	Lys	Cys	
					175					180					185	
tac aca ttt aac tct ggc gct gat ggg gca gag ctg ctc acc act act															627	
Tyr	Thr	Phe	Asn	Ser	Gly	Ala	Asp	Gly	Ala	Glu	Leu	Leu	Thr	Thr	Thr	
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agg ggt ggc atg ggc aat ggg ctg gac atc atg ctg gac gtg cag cag															675	
Arg	Gly	Gly	Met	Gly	Asn	Gly	Leu	Asp	Ile	Met	Leu	Asp	Val	Gln	Gln	
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gag gaa tat cta cct gtg tgg agg gac aat gag gag acc ccg ttt gag															723	
Glu	Glu	Tyr	Leu	Pro	Val	Trp	Arg	Asp	Asn	Glu	Glu	Thr	Pro	Phe	Glu	
					220					225					230	
gtg ggg atc cga gtg cag atc cac agc cag gag gag ccg ccc atc atc															771	
Val	Gly	Ile	Arg	Val	Gln	Ile	His	Ser	Gln	Glu	Glu	Pro	Pro	Ile	Ile	
					235					240					245	
gat cag ctg ggc ttg ggg gtg tcc ccg ggc tac cag acc ttt gtt tct															819	

Asp Gln Leu Gly Leu Gly Val Ser Pro Gly Tyr Gln Thr Phe Val Ser			
255	260	265	
tgc cag cag cag ctg agc ttc ctg cca ccg ccc tgg ggc gat tgc			867
Cys Gln Gln Gln Leu Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys			
270	275	280	
agt tca gca tct ctg aac ccc aac tat gag cca gag ccc tct gat ccc			915
Ser Ser Ala Ser Leu Asn Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro			
285	290	295	
cta ggc tcc ccc agc ccc agc ccc agc cct ccc tat acc ctt atg ggg			963
Leu Gly Ser Pro Ser Pro Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly			
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tgt cgc ctg gcc tgc gaa acc cgc tac gtg gct cg ^g aag tgc ggc tgc			1011
Cys Arg Leu Ala Cys Glu Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys			
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cga atg gtg tac atg cca ggc gac gtg cca gtg tgc agc ccc cag cag			1059
Arg Met Val Tyr Met Pro Gly Asp Val Pro Val Cys Ser Pro Gln Gln			
335	340	345	
tac aag aac tgt gcc cac ccg gcc ata gat gcc atc ctt cgc aag gac			1107
Tyr Lys Asn Cys Ala His Pro Ala Ile Asp Ala Ile Leu Arg Lys Asp			
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Ser Cys Ala Cys Pro Asn Pro Cys Ala Ser Thr Arg Tyr Ala Lys Glu			
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Leu Ser Met Val Arg Ile Pro Ser Arg Ala Ala Arg Phe Leu Ala			
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cg ^g aag ctc aac cgc agc gag gcc tac atc g ^g g ^g aac gtg ctg gcc			1251
Arg Lys Leu Asn Arg Ser Glu Ala Tyr Ile Ala Glu Asn Val Leu Ala			
395	400	405	410
ctg gac atc ttc ttt gag gcc ctc aac tat gag acc gtg gag cag aag			1299
Leu Asp Ile Phe Phe Glu Ala Leu Asn Tyr Glu Thr Val Glu Gln Lys			
415	420	425	
aag gcc tat gag atg tca gag ctg ctt ggt gac att ggg ggc cag atg			1347
Lys Ala Tyr Glu Met Ser Glu Leu Leu Gly Asp Ile Gly Gly Gln Met			
430	435	440	
ggc ctt ttc atc ggg gcc agc ctg ctc acc atc ctc gag atc cta gac			1395

Gly Leu Phe Ile Gly Ala Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp				
445	450	455		
tac ctc tgt gag gtg ttc cga gac aag gtc ctg gga tat ttc tgg aac				1443
Tyr Leu Cys Glu Val Phe Arg Asp Lys Val Leu Gly Tyr Phe Trp Asn				
460	465	470		
cga cag cac tcc caa agg cac tcc agc acc aat ctg ctt cag gaa ggg				1491
Arg Gln His Ser Gln Arg His Ser Ser Thr Asn Leu Leu Gln Glu Gly				
475	480	485	490	
ctg ggc agc cat cga acc caa gtt ccc cac ctc agc ctg ggc ccc aga				1539
Leu Gly Ser His Arg Thr Gln Val Pro His Leu Ser Leu Gly Pro Arg				
495	500	505		
cct ccc acc cct ccc tgt gcc gtc acc aag act ctc tcc gcc tcc cac				1587
Pro Pro Thr Pro Pro Cys Ala Val Thr Lys Thr Leu Ser Ala Ser His				
510	515	520		
cgc acc tgc tac ctt gtc aca cag ctc tagacctgct gtctgtgtcc				1634
Arg Thr Cys Tyr Leu Val Thr Gln Leu				
525	530			
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Phe Gly Pro Gly Ser Leu Ser Leu Arg Arg Gly Met Trp Ala Ala Ala				
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Val Val Leu Ser Val Ala Thr Phe Leu Tyr Gln Val Ala Glu Arg Val				
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Arg Tyr Tyr Arg Glu Phe His His Gln Thr Ala Leu Asp Glu Arg Glu				
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Ser His Arg Leu Val Phe Pro Ala Val Thr Leu Cys Asn Ile Asn Pro
85 90 95

Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly Ser
100 105 110

Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Phe Leu Arg Ala
115 120 125

Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr Phe
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Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Asp Asp Met
145 150 155 160

Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro Cys Gly Pro Glu Asn Phe
165 170 175

Thr Thr Ile Phe Thr Arg Met Gly Lys Cys Tyr Thr Phe Asn Ser Gly
180 185 190

Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr Arg Gly Gly Met Gly Asn
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Gly Leu Asp Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro Val
210 215 220

Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val Gln
225 230 235 240

Ile His Ser Gln Glu Glu Pro Pro Ile Ile Asp Gln Leu Gly Leu Gly
245 250 255

Val Ser Pro Gly Tyr Gln Thr Phe Val Ser Cys Gln Gln Gln Leu
260 265 270

Ser Phe Leu Pro Pro Trp Gly Asp Cys Ser Ser Ala Ser Leu Asn
275 280 285

Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro Ser Pro
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Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly Cys Arg Leu Ala Cys Glu
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Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Val Tyr Met Pro
325 330 335

Gly Asp Val Pro Val Cys Ser Pro Gln Gln Tyr Lys Asn Cys Ala His			
340	345	350	
Pro Ala Ile Asp Ala Ile Leu Arg Lys Asp Ser Cys Ala Cys Pro Asn			
355	360	365	
Pro Cys Ala Ser Thr Arg Tyr Ala Lys Glu Leu Ser Met Val Arg Ile			
370	375	380	
Pro Ser Arg Ala Ala Ala Arg Phe Leu Ala Arg Lys Leu Asn Arg Ser			
385	390	395	400
Glu Ala Tyr Ile Ala Glu Asn Val Leu Ala Leu Asp Ile Phe Phe Glu			
405	410	415	
Ala Leu Asn Tyr Glu Thr Val Glu Gln Lys Lys Ala Tyr Glu Met Ser			
420	425	430	
Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala			
435	440	445	
Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu Val Phe			
450	455	460	
Arg Asp Lys Val Leu Gly Tyr Phe Trp Asn Arg Gln His Ser Gln Arg			
465	470	475	480
His Ser Ser Thr Asn Leu Leu Gln Glu Gly Leu Gly Ser His Arg Thr			
485	490	495	
Gln Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Pro Pro Cys			
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<223> "Xaa = unidentified amino acid."

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Ser

<210> 4
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<212> DNA
<213> Artificial Sequence

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Oligonucleotide Primer

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<212> DNA
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Oligonucleotide Primer

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21